IN THE CLAIMS:

All claim amendments and cancellations are made without prejudice or disclaimer. Please amend the claims as follows:

1. (Currently amended) A genetically engineered construct comprising a gene-mutated equine infectious anemia virus(EIAV) genome comprising two (2) redundant stop codons in the EIAV's S2 open reading frame and a deletion wherein said virus lacks the ability to express the mutated gene's protein *in vivo* and wherein said lack of expression can be used to differentiate vaccinated from non-vaccinated or infected mammals.

2. (Canceled)

3. (Currently amended) The genetically engineered construct of Claim 1 wherein the two stop codons are engineered into the proviral DNA of $EIAV_{UK}$ at the EIAV's S2 amino acids G^5 and G^{18}.

4. (Currently amended) The genetically engineered construct of Claim 1 wherein said stop codon does not affect normal expression of the envelope protein.

5. (Currently amended) The genetically engineered construct of Claim 1 wherein the deletion is a deletion of between 6 and 25 base pairs.

6. (Currently amended) The genetically engineered construct of Claim 5 wherein the said deletion is located at least 7 base pairs downstream of the stop codon of the second coding region of TAT.

7. (Currently amended) The genetically engineered construct according to Claim 5 wherein said deletion does not interrupt the splice donor 2 site downstream of the stop codon of

the second coding region of TAT and upstream of the initiation codon of the EIAV's S2 open reading frame.

8. (Currently amended) The genetically engineered construct according to Claim 5 wherein said deletion is upstream of the envelope coding region.

9. (Currently amended) The genetically engineered construct of Claim 5 wherein the deletion is 9 base pairs.

10. (Currently amended) The genetically engineered construct of Claim 3 wherein generation of the stop codon at G^5 further comprises the insertion of a restriction endonuclease site whereby the restriction endonuclease is a molecular marker for differentiating between wildtype EIAV and the gene-mutated EIAV.

11-13 (Canceled)

14. (Currently amended) A genetically engineered construct comprising a gene-mutated EIAV genome comprising two (2) redundant stop codons wherein the two redundant stop codons are inserted into the EIAV's S2 open reading frame and engineered into the proviral DNA of $EIAV_{UK}$ at the EIAV's S2 amino acids G^5 and G^{18} and a deletion comprising 9 base pairs outside the envelope open reading frame.

15. (Currently amended) A genetically engineered construct comprising a gene-mutated EIAV genome comprising two (2) redundant stop codons wherein the two redundant stop codons are inserted into the EIAV's S2 open reading frame and engineered into the proviral DNA of the EIAV's $EIAV_{UK}$ at S2 amino acids G^5 and G^{18} and a deletion comprising between 6 and 25 base pairs outside the envelope open reading frame.

16. (Currently amended) The genetically engineered construct of Claim 15 wherein said virus

lacks the ability to express the mutated gene protein *in vivo* and wherein said lack of expression can be used to differentiate vaccinated from non-vaccinated or infected mammals.